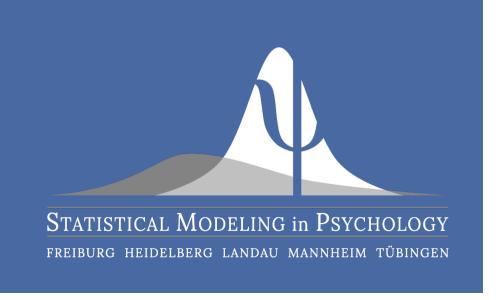




SMiP Core Course: Foundations of Statistical Modeling II

Multinomial Processing Tree Modeling: Basic Methods and Recent Advances

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Multinomial Processing Tree (MPT) Modeling, Part 1: Basics

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1) Basics

- 1.1) Introduction to standard MPT models
- 1.2) Examples
- 1.3) Model development
- 1.4) Formal model structure
- 1.5) Identifiability
- 1.6) Parameter estimation
- 1.7) Model assessment
- 1.8) Selected literature

1.1) Introduction to standard MPT models

- Required type of data:
- Standard multinomial models are tailored to discrete (i.e., categorical) data.
- Psychological data are typically discrete in nature (e.g., yes/no responses, correct/incorrect judgments, ratings, choices, ...).
- If not, they can often be transformed into discrete data
 - Response times: Categorization into bins
 - Numerical judgments: Rank-orders of judgments
- Hence, many psychological paradigms generate frequency data that are appropriate for MPT modeling.

1.1) Introduction to standard MPT models

- Distributional assumptions:
- Standard MPT models assume that observations are sampled independently from
 - one multinomial distribution (simple multinomial model)
 - several multinomial distributions (joint multinomial model)
- This includes simple and joint binomial models as special cases.
- The frequency data structure can be univariate or multivariate.

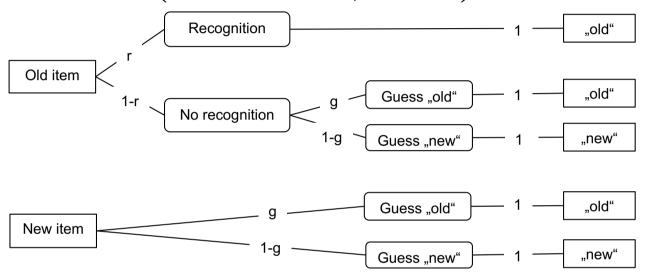
MPT models ...

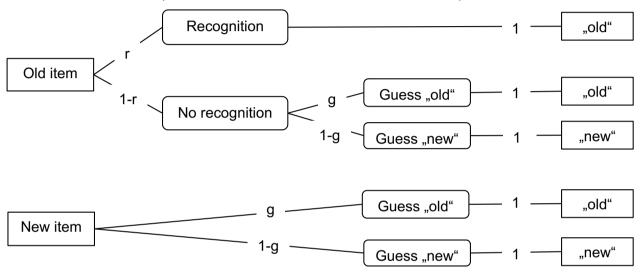
- ... provide explanations of observed frequency data in terms of basic parameters with clear-cut psychological interpretations;
- ... these parameters represent probabilities of latent psychological processes (or latent psychological states) underlying human behavior;
- ... in other words, these models measure the contributions of different psychological processes to frequencies of observable behaviors.
- In this sense, multinomial models allow for a "measurement of cognitive processes" (Riefer & Batchelder, 1988)

1.2) Examples

A very simple example:

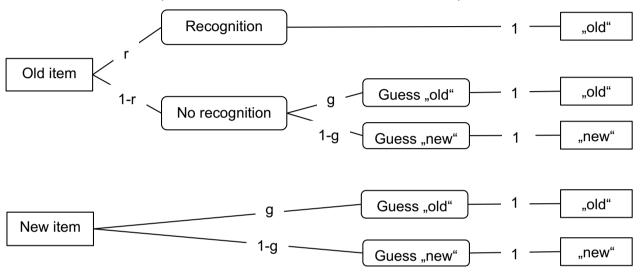
- Paradigm:
 - Yes-No recognition test
- Two Conditions:
 - Old Items
 - New Items
- Categorical (dichotomous) dependent variable:
 - "Old" vs. "New" Judgment





Model equations:

$$p(,,\text{old"} \mid \text{old item}) = r + (1-r) \cdot g$$



Model equations:

$$p(,,old" | old item) = r + (1-r) \cdot g$$

 $p(,,old" | new item) = g$

B) Separating storage and retrieval in long-term memory

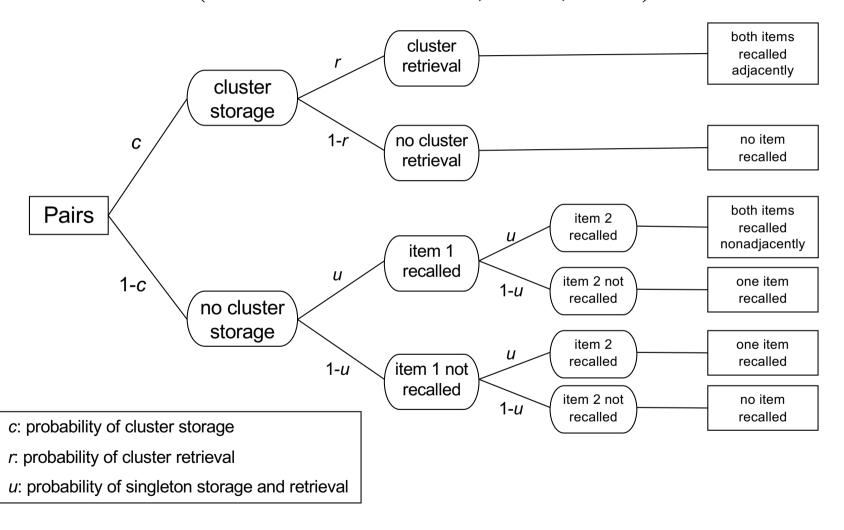
- Empirical Paradigm:
 - Free recall of word list consisting of
 - Word pairs (e.g. "chair" und "table")
 - Singletons (e.g., ,,rose" and no other flower).
 - "Primacy—" and "Recency–Buffer".
- Two distributions of responses:
 - pairs
 - singletons

Scoring of responses

- Observation categories
 - For word pairs:
 - E1 both words recalled adjacently
 - E2 both words recalled nonadjacently
 - E3 one word recalled
 - E4 no word recalled
 - For singletons:
 - F1 Recalled
 - F2 Not recalled

Pair-Clustering Model

(Batchelder & Riefer, 1980, 1986)



Model equations

- Word pairs:
- $p(\mathbf{E}_1) = c \cdot r$
- $p(E_2) = (1 c) \cdot u^2$
- $p(E_3) = (1 c) \cdot 2 \cdot u \cdot (1 u)$
- $p(E_4) = c \cdot (1 r) + (1 c) \cdot (1 u)^2$
- Singletons:
- $p(F_1) = u$
- $p(F_2) = 1 u$

1.3) Model development

- Preliminary summary:
- Select a paradigm (e.g., a task)
- Define the conditions of the paradigm
- Define the category system for each condition
- List relevant processes/parameters
- Construct theoretically reasonable processing branches ("trees") for each condition
- Derive corresponding model equations.
- General rules:
 - As simple as possible!!
 - Ignore unlikely events

Recommendation

- When developing a new model, make notes of potentially problematic assumptions:
 - Cluster retrieval is an ,,all or nothing" process;
 - All words are equally difficult;
 - Words of a pair that is not stored as a cluster are stored and retrieved in a stochastically independent fashion;
 - Words of a pair that is not stored as a cluster are never recalled adjacently.
- Design your experiment in a way such that these assumptions are likely to be true.
- If the model misfits the data, consider these issues again and try to revise the model.

1.4) Formal model structure

- Multinomial models
- Parameterized multinomial models
- Multinomial processing tree (MPT) models
- Processing-tree representation of MPT models

Multinomial Models

- a) One condition (simple multinomial model)
- One variable with J categories and sample frequencies $n_1, n_2, ..., n_j, ..., n_J$.
- $\pi = (p_1, p_2, ..., p_J)$ is the vector of category probabilities.
- Given independent sampling, the sample frequencies follow a multinomial distribution:

$$p_{N,\pi}(n_1,n_2,...,n_J) = \frac{N}{n_1! n_2! ... n_J!} p_1^{n_1} p_2^{n_2} ... p_J^{n_J}$$

b) Several conditions (joint multinomial model)

- In each condition k (k = 1, ..., K), one categorical variable with J(k) categories is observed.
- For each of the *K* conditions, a simple multinomial model holds.
- Given independence between conditions, the overall probability of the sample frequencies across conditions is

$$p = \prod_{k=1}^{K} p_{N(k),\pi(k)}(n_{1(k)}, n_{2(k)}, ..., n_{J(k)})$$

Parameterized Multinomial Models

- The category probabilities p_1, p_2 etc. are rewritten as functions of latent parameters $\theta_1, \theta_2, ..., \theta_S$
- Thus, in case of a simple multinomial model we have

$$- p_1 = f_1(\theta_1, \theta_2, ..., \theta_S)$$

$$- p_2 = f_2(\theta_1, \theta_2, ..., \theta_S)$$

$$-$$

$$- p_J = f_J(\theta_1, \theta_2, ..., \theta_S)$$

- These equations are called model equations.
- The set of possibles values of S latent parameters is called "parameter space" Ω of the model.

Multinomial Processing Tree (MPT) Models

- MPT models form a subclass of parameterized multinomial models.
- Additional assumptions:
- 1) Each θ_s is in [0, 1]

Multinomial Processing Tree (MPT) Models

- MPT models form a subclass of parameterized multinomial models.
- Additional assumptions:
- 1) Each θ_s is in [0, 1]
- 2) Structure of the model equations (Hu & Batchelder, 1994):

$$p_{j} = \sum_{i=1}^{I(j)} c_{ij} \prod_{s=1}^{S} \mathbf{\theta}_{s}^{a_{ijs}} \cdot (1 - \mathbf{\theta}_{s})^{b_{ijs}}, \qquad \sum_{j=1}^{J} p_{j} = 1, \qquad \mathbf{\theta}_{s} \in [0, 1]$$

where s: Parameter index

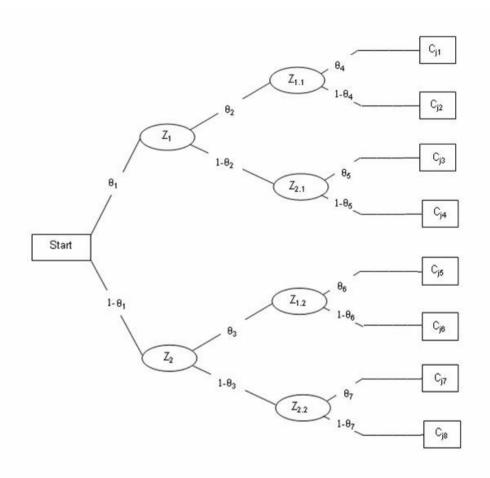
j : Category index

i : *B*ranch index

 c_{ij} : positive real number

 a_{ijs} , b_{ijs} : nonnegative integer number (often 0 or 1)

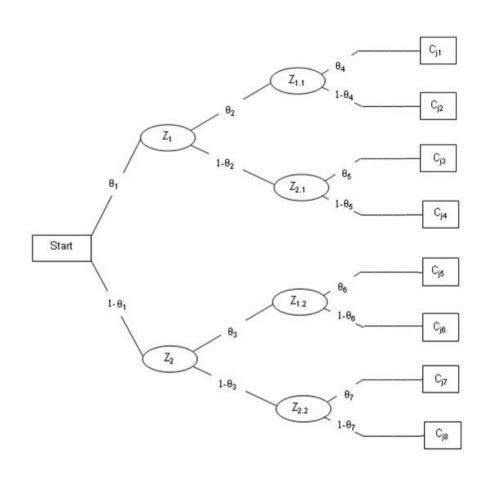
Binary probabilistic event trees can always be translated in MPT-model equations:



... as an aside ...

- Although any binary processing tree diagram uniquely determines a system of MPT model equations ...
- ... it is not true that any system of MPT model equations uniquely determines a specific processing tree diagram.
- Counter examples:
 - Level switching in independence models
 - Category switching given identical branch probabilities

Example: Assume θ_1 = .5, θ_2 = θ_3 , θ_4 = θ_6



Another counter example is this MPT model:

$$p_1(\theta) = \theta^3$$

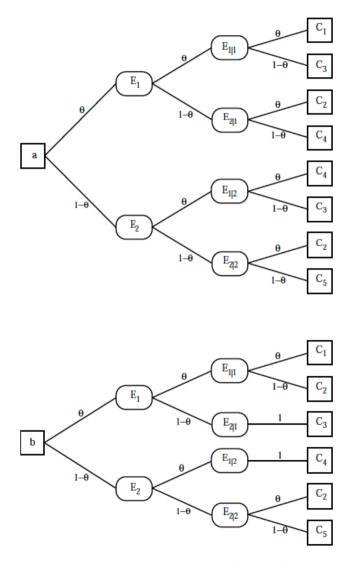
$$p_2(\theta) = \theta \cdot (1 - \theta)$$

$$p_3(\theta) = \theta \cdot (1 - \theta)$$

$$p_4(\theta) = \theta \cdot (1 - \theta)$$

$$p_5(\theta) = (1 - \theta)^3$$

Two different processing trees compatible with the model on the previous slide:



MPT Workshop (Erdfelder & Heck), Day 1, Part 1

1.5) Identifiability

Any MPT model equation system

$$p_{j} = \sum_{i=1}^{I(j)} c_{ij} \prod_{s=1}^{S} \theta_{s}^{a_{ijs}} \cdot (1 - \theta_{s})^{b_{ijs}}, \qquad \sum_{j=1}^{J} p_{j} = 1, \qquad \theta_{s} \in [0, 1]$$

where s: Parameter index

j : Category index

i: Branch index

 c_{ii} : positive real number

 a_{ijs} , b_{ijs} : nonnegative integer number (often 0 or 1)

defines a mapping $f: \Omega \rightarrow P$

Parameter Space and Data Space

- Ω is called "Parameter Space":
 - = Set of all possible parameter vectors
- P is called "Data Space" (more precisely: space of category probabilities)
 - = Set of all possible category probability vectors

Identifiability of an MPT model

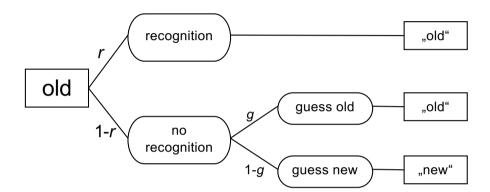
Definition (global identifiability):

An MPT model is globally identified if f is one-to-one.

Definition (local identifiability):

An MPT model is locally identified if f is one-to-one in the neighborhood of θ_0 in Ω .

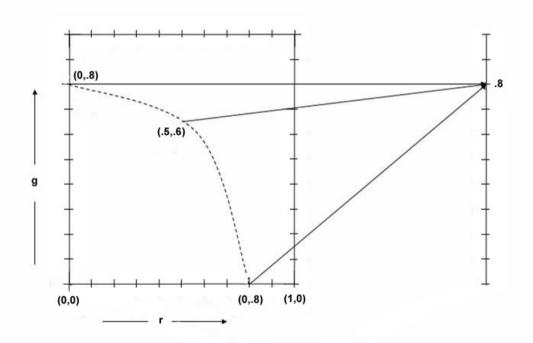
One-High-Threshold recognition model (Blackwell, 1953)



r. probability of recognition

g: probability of guessing old given recognition

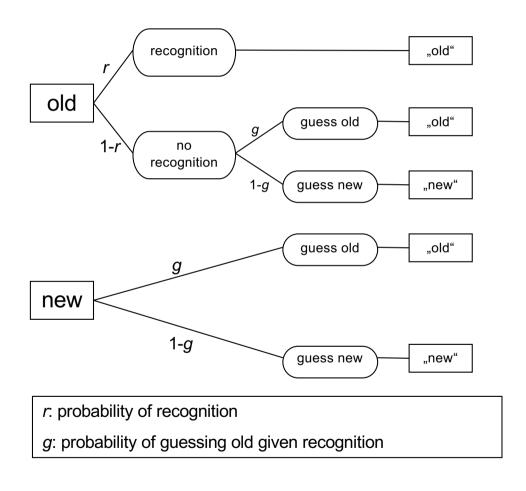
Example 1 (nonidentifiability)



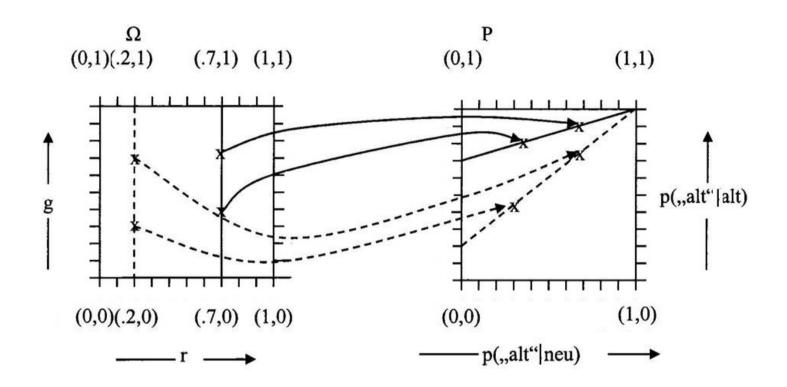
- One-high-Threshold-Modell limited to old items:
 - p("alt" | old item) = $r + (1-r) \cdot g$
- Model is not identified.

One-High-Threshold recognition model

(Blackwell, 1953)



Example 2 (identifiability)



- One-high-Threshold-Model (old and new items)
 - p("alt" | old item) = $r + (1-r) \cdot g$
 - $p(,,alt" \mid new item) = g$
- Model is globally identified.

Two important theorems:

• "Observable branches":

A model is always globally identified if each of its branches terminates in a unique empirical category (Hu & Batchelder, 1994).

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• ,,No more parameters than degrees of freedom in the data":

A necessary but not sufficient condition of identifiability is

$$S \leq \sum_{k=1}^K (J(k)-1).$$

Jacobian Matrix

- Jacobian: Matrix of the 1st partial derivates of the model equations with respect to parameters θ_s , s = 1, ... S.
- r: maximum rank of the Jacobian across Ω
- If r < S, then the model is neither locally nor globally identified.
- If r = S, then the model is locally identified (but not necessarily globally).

Remedies for nonidentifiable models

- Parameter constraints
 - Parameter fixations ($\theta_s = c$, with c = constant)
 - Equality constraints ($\theta_s = \theta_{s'}$)
- Increase the number of empirical categories
 - Add more conditions that require no (or few) additional parameters
 - Simple recipe that often works: Selective manipulations of parameters

1.6) Parameter Estimation

Find a parameter vector $\theta = (\theta_1, ..., \theta_s, ..., \theta_s), \theta \in \Omega$, such that the distance between the sample frequencies $n_1, n_2, ..., n_J$ and the expected category frequencies under the model, $N \cdot p_1(\theta), N \cdot p_2(\theta), ..., N \cdot p_J(\theta)$, becomes a minimum.

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Which distance measure?

1.6) Parameter Estimation

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Which distance measure?

The likelihood ratio statistic G^2 and Pearson's χ^2 are used most often:

$$G^{2}(\theta) = 2\sum_{j=1}^{J} n_{j} \ln \left(\frac{n_{j}}{N \cdot p_{j}(\theta)} \right) \qquad \chi^{2}(\theta) = \sum_{j=1}^{J} \frac{\left[n_{j} - N \cdot p_{j}(\theta) \right]^{2}}{N \cdot p_{j}(\theta)}$$

Both distance measures are special cases of the Power-Divergence-family (PD_{λ} -Statistics) (Read & Cressie, 1988):

$$s_{\lambda} = \frac{2}{\lambda(\lambda+1)} \sum_{k=1}^{k} \sum_{i=1}^{J(k)} n_{j(k)} \cdot \left[\left(\frac{n_{j(k)}}{e_{j(k)}} \right)^{\lambda} - 1 \right]$$

Note that:

Pearson-
$$\chi^2$$
 = $S_{\lambda=1}$
Likelihood-ratio- G^2 = $\lim_{\lambda \to 0} S_{\lambda}$.

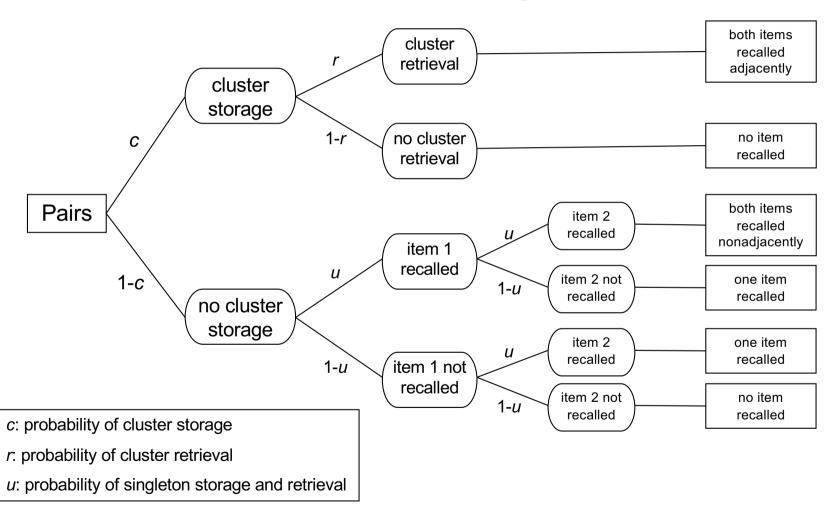
What is the best estimation method?

- All S_{λ} -estimates have the same asymptotic properties:
 - Consistent, efficient, asympotically unbiased
 - (multivariate) normal sampling distributions
- Choosing λ =0 (i.e., minimizing G^2) provides Maximum Likelihood (ML) estimates:
 - Sample frequencies have highest likelihood
 - Standard method in typical applications
- All S_{λ} -estimates are easily implemented using the robust Expectation-Maximization (EM) estimation algorithm.

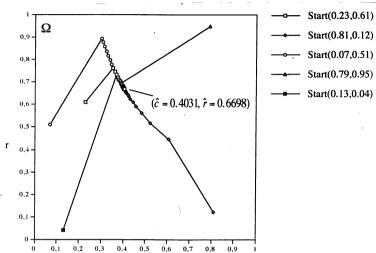
Expectation-Maximization-(EM) Algorithm

- 1) Choose a (random) start vector θ_i .
- 2) **E**(xpectation)-Step:
 - Estimate the expected frequencies of the branches given θ_i and the observed category frequencies $n_{i(k)}$
- 3) M(aximization)-Step:
 - Let i = i + 1
 - Compute new S_{λ} estimates θ_i given the expected frequencies from step 2)
- 4) Convergence ?
 - If $Abs(\theta_i \theta_{i-1}) > Criterion for some i, go back to step 2)$
- 5) Otherwise accept θ_i as final parameter estimates $\hat{\boldsymbol{\theta}}$

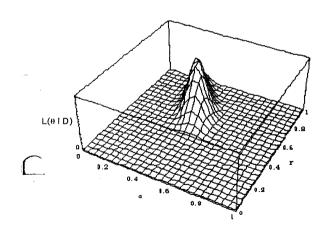
Application of EM algorithm to Pair-Clustering Model



Graphical Illustration of the EM-Algorithm applied to c and r in storage-retrieval model:



EM paths in Ω for $\lambda = 0$, given five different starting values (simulated data).

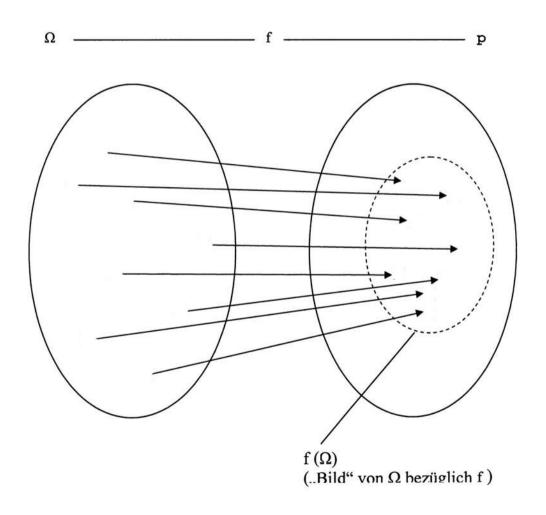


Likelihood (y-axis) as a function of *c* und *r* given the same simulated data as before.

Bottom line

- Use G^2 -minimization (= likelihood maximization) as the default estimation method.
- Repeat the estimation process several times using random start values to make sure that you really found a global maximum of the likelihood function.

1.7) Model assessment



How to test H_0 : $\pi \in f(\Omega)$?

Options:

Pearson
$$\chi^2 = \sum_{k=1}^K \sum_{j=1}^{J(k)} (n_{j(k)} - e_{j(k)})^2 / e_{j(k)}$$
,

or

Likelihood - ratio -
$$G^2 = 2 \cdot \sum_{k=1}^K \sum_{j=1}^{J(k)} n_{j(k)} \cdot \ln(n_{j(k)} / e_{j(k)});$$

with $e_{j(k)} = p_{j(k)}(\hat{\boldsymbol{\theta}}) \cdot N(k)$

Both statistics are special cases of Read und Cressies (1988) "Power Divergence" – Statistics:

$$S_{\lambda} = \frac{2}{\lambda(\lambda+1)} \sum_{k=1}^{k} \sum_{j=1}^{J(k)} n_{j(k)} * \left[\left(\frac{n_{j(k)}}{e_{j(k)}} \right)^{\lambda} - 1 \right]$$

Again:

Pearson- $\chi^2 = S_{\lambda=1}$

Likelihood-ratio- $G^2 = \lim_{\lambda \to 0} S_{\lambda}$.

All S_{λ} – Statistics are asymptotically (i.e., for $N \rightarrow oo$) chi-square distributed under H_0 (i.e., the model holds) with

df =
$$\sum_{k=1}^{K} (J(k)-1)-S$$
.

What is the best goodness-of-fit statistic?

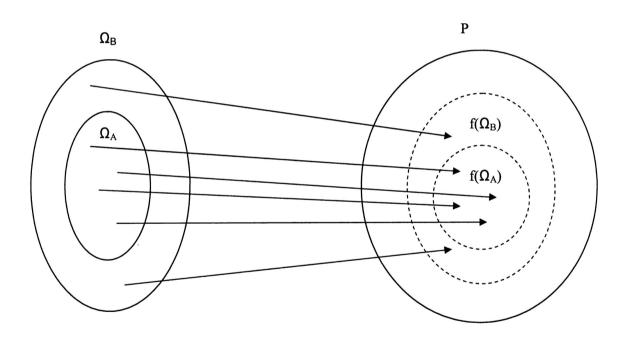
- In case of very small sample sizes, $S_{\lambda=2/3}$ outperforms other S_{λ} -statistics (such as $G^2 = S_{\lambda=0}$) in terms of accuracy of Chi-square approximation (cf. Read & Cressie, 1988).
- However, very small samples are typically less of a problem in MPT model applications (unless models are tested for single participants).
- Given the fact that G^2 is a by-product of ML-parameter estimation, G^2 can be recommended for moderate to large sample sizes.
- However, you cannot choose G^2 in case of samples with zero cells.
- Remedies: 1) Ignore 0 cells, 2) add constant ε to all counts

Model comparisons

- Assume that model B (M_B) holds for your data: $G^2(M_B)$ is not significant.
- Then often M_B is compared to an alternative model A (M_A) that is a special case of M_B .
- M_A is obtained by applying a parameter restriction to M_B , e.g., an equality constraint or a parameter fixation.
- How to decide whether M_A fits the data worse than M_B ?

Model M_A as a special case of M_B :

Illustration of model-specific mapping of Ω_A and Ω_B in P.



This is called a "hierarchical model family".

Model comparisons in hierarchical model families

- If both M_A and M_B hold then
 - G²_A is chi-square distributed with df_A
 - G²_B is chi-square distributed with df_B
 - ΔG^2_{A-B} : = $G^2_A G^2_B$ is chi-square distributed with $df_{A-B} = df_A df_B$.
- In other words, G^2 is additive (irrespective of N): $G^2_A = G^2_B + \Delta G^2_{A-B}$
- This additivity property does not hold for other PD_{λ} -stats.
- Using ΔG^2_{A-B} , it is easy to compare different models in a hierarchical model family using chi-square tests
- This is perhaps the strongest argument for relying on G^2 for purposes of model fitting and testing.

Model comparisons in nonhierarchical model families

- Unfortunately, ΔG^2_{A-B} : = $G^2_A G^2_B$ cannot be used in nonhierarchical model families.
- How to proceed then?

Information-theoretic measures of goodness-of-fit

- Akaike Information Criterion (AIC):
 - $AIC(M_0) = -2 \cdot ln(L(\theta; \mathbf{y})) + 2 \cdot S$
 - $-\Delta AIC(M_0) = AIC(M_0) AIC(sat.) = G^2(M_0) 2 \cdot df(M_0)$
- Bayesian Information Criterion (BIC):
 - $-\operatorname{BIC}(\mathbf{M}_0) = -2 \cdot \ln(\operatorname{L}(\boldsymbol{\theta}; \mathbf{y})) + S \cdot \ln(N)$
 - $-\Delta BIC(M_0) = BIC(M_0)-BIC(sat.) = G^2(M_0)-df(M_0)\cdot ln(N)$
- Rule:
 - Choose the model with the smaller AIC / BIC
- Recommendation:
 - Fit is fine if $\triangle AIC$ or $\triangle BIC < 0$.

1.8) Selected literature

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